



SEQUENCE LISTING

<110> Evans, Ronald M.
Forman, Barry M.

<120> SELECTIVE MODULATORS OF PEROXISOME
PROLIFERATOR ACTIVATED RECEPTOR-GAMMA, AND METHODS FOR THE
USE THEREOF

<130> SALK1470-2

<140> 09/155,252

<141> 1998-09-21

<150> PCT/US96/05465

<151> 1996-04-18

<160> 7

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2005

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (352)...(1776)

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| ggaggacgcg | gaagaagaga | cctggggcgc | tgcctgggggt | attgggtcgc | gcgcagtgag | 120 |
| gggaccgagt | gtgacgacaa | ggtgaccggg | ctgaggggac | gggctgagga | gaagtacacac | 180 |
| tctgacagga | gcctgtgaga | ccaacagcct | gacgggggtct | cggttgaggg | gacgcggggt | 240 |
| gagaagtcac | gttctgacag | gactgtgtga | cagacaagat | ttgaaagaag | cgggtgaacca | 300 |
| ctgatattca | ggacattttt | aaaaacaaga | ctacccttta | ctgaaattac | c atg gtt | 357 |
| | | | | | Met Val | |

1

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gac | aca | gag | atg | cca | ttc | tgg | ccc | acc | aac | ttc | gga | atc | agc | tct | gtg | 405 |
| Asp | Thr | Glu | Met | Pro | Phe | Trp | Pro | Thr | Asn | Phe | Gly | Ile | Ser | Ser | Val | |
| 5 | | | | | | | 10 | | | | | 15 | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gac | ctc | tcc | gtg | atg | gaa | gac | cac | tcg | cat | tcc | ttt | gac | atc | aag | ccc | 453 |
| Asp | Leu | Ser | Val | Met | Glu | Asp | His | Ser | His | Ser | Phe | Asp | Ile | Lys | Pro | |
| 20 | | | | | | 25 | | | | | 30 | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ttt | acc | aca | gtt | gat | ttc | tcc | agc | att | tct | gct | cca | cac | tat | gaa | gac | 501 |
| Phe | Thr | Thr | Val | Asp | Phe | Ser | Ser | Ile | Ser | Ala | Pro | His | Tyr | Glu | Asp | |
| 35 | | | | | 40 | | | | | 45 | | | | 50 | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| att | cca | ttc | aca | aga | gct | gac | cca | atg | gtt | gct | gat | tac | aaa | tat | gac | 549 |
| Ile | Pro | Phe | Thr | Arg | Ala | Asp | Pro | Met | Val | Ala | Asp | Tyr | Lys | Tyr | Asp | |
| | | | | 55 | | | | | 60 | | | | | 65 | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ctg | aag | ctc | caa | gaa | tac | caa | agt | gcg | atc | aaa | gta | gaa | cct | gca | tct | 597 |
| Leu | Lys | Leu | Gln | Glu | Tyr | Gln | Ser | Ala | Ile | Lys | Val | Glu | Pro | Ala | Ser | |
| | | | 70 | | | | | 75 | | | | | | 80 | | |

| | |
|-----------------------------------------------------------------|------|
| cca cct tat tat tct gaa aag acc cag ctc tac aac agg cct cat gaa | 645 |
| Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Arg Pro His Glu | |
| 85 90 95 | |
| gaa cct tct aac tcc ctc atg gcc att gag tgc cga gtc tgt ggg gat | 693 |
| Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys Gly Asp | |
| 100 105 110 | |
| aaa gca tca ggc ttc cac tat gga gtt cat gct tgt gaa gga tgc aag | 741 |
| Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys | |
| 115 120 125 130 | |
| ggg ttt ttc cga aga acc atc cga ttg aag ctt att tat gat agg tgt | 789 |
| Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg Cys | |
| 135 140 145 | |
| gat ctt aac tgc cgg atc cac aaa aaa agt aga aat aaa tgt cag tac | 837 |
| Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys Gln Tyr | |
| 150 155 160 | |
| tgt cgg ttt cag aag tgc ctt gct gtg ggg atg tct cac aat gcc atc | 885 |
| Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn Ala Ile | |
| 165 170 175 | |
| agg ttt ggg cgg atg cca cag gcc gag aag gag aag ctg ttg gcg gag | 933 |
| Arg Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu Leu Ala Glu | |
| 180 185 190 | |
| atc tcc agt gat atc gac cag ctg aac cca gag tct gct gat ctg cga | 981 |
| Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp Leu Arg | |
| 195 200 205 210 | |
| gcc ctg gca aag cat ttg tat gac tca tac ata aag tcc ttc ccg ctg | 1029 |
| Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser Phe Pro Leu | |
| 215 220 225 | |
| acc aaa gcc aag gcg agg gcg atc ttg aca gga aag aca acg gac aaa | 1077 |
| Thr Lys Ala Lys Ala Arg Ala Ile Leu Thr Gly Lys Thr Thr Asp Lys | |
| 230 235 240 | |
| tca cca ttt gtc atc tac gac atg aat tcc tta atg atg gga gaa gat | 1125 |
| Ser Pro Phe Val Ile Tyr Asp Met Asn Ser Leu Met Met Gly Glu Asp | |
| 245 250 255 | |
| aaa atc aag ttc aaa cat atc acc ccc ctg cag gag cag agc aaa gag | 1173 |
| Lys Ile Lys Phe Lys His Ile Thr Pro Leu Gln Glu Gln Ser Lys Glu | |
| 260 265 270 | |
| gtg gcc atc cga att ttt caa ggg tgc cag ttt cga tcc gta gaa gcc | 1221 |
| Val Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val Glu Ala | |
| 275 280 285 290 | |
| gtg caa gag atc aca gag tat gcc aaa aat atc cct ggt ttc att aac | 1269 |
| Val Gln Glu Ile Thr Glu Tyr Ala Lys Asn Ile Pro Gly Phe Ile Asn | |
| 295 300 305 | |
| ctt gat ttg aat gac caa gtg act ctg ctc aag tat ggt gtc cat gag | 1317 |
| Leu Asp Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val His Glu | |
| 310 315 320 | |

atc atc tac acg atg ctg gcc tcc ctg atg aat aaa gat gga gtc ctc 1365
 Ile Ile Tyr Thr Met Leu Ala Ser Leu Met Asn Lys Asp Gly Val Leu
 325 330 335

atc tca gag ggc caa gga ttc atg acc agg gag ttc ctc aaa agc ctg 1413
 Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys Ser Leu
 340 345 350

cgg aag ccc ttt ggt gac ttt atg gag cct aag ttt gag ttt gct gtg 1461
 Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe Ala Val
 355 360 365 370

aag ttc aat gca ctg gaa tta gat gac agt gac ttg gct ata ttt ata 1509
 Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe Ile
 375 380 385

gct gtc att att ctc agt gga gac cgc cca ggc ttg ctg aac gtg aag 1557
 Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn Val Lys
 390 395 400

ccc atc gag gac atc caa gac aac ctg ctg cag gcc ctg gaa ctg cag 1605
 Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu Leu Gln
 405 410 415

ctc aag ctg aat cac cca gag tcc tct cag ctg ttc gcc aag gtg ctc 1653
 Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys Val Leu
 420 425 430

cag aag atg aca gac ctc agg cag atc gtc aca gag cac gtg cag cta 1701
 Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val Gln Leu
 435 440 445 450

ctg cat gtg atc aag aag aca gag aca gac atg agc ctt cac ccc ctg 1749
 Leu His Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu His Pro Leu
 455 460 465

ctc cag gag atc tac aag gac ttg tat tagcaggaaa gtcccacccg 1796
 Leu Gln Glu Ile Tyr Lys Asp Leu Tyr
 470 475

ctgacaacgt gttccttcta ttgattgcac tattatitttg aggggaaaaaa atctgacacc 1856
 taagaaattt actgtgaaaa agcattttaa aacaaaaagt tttagaacat gatctatttt 1916
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<213> Mus musculus

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 20 25 30
 Lys Pro Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Ala Pro His Tyr
 35 40 45
 Glu Asp Ile Pro Phe Thr Arg Ala Asp Pro Met Val Ala Asp Tyr Lys
 50 55 60

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Asp | Leu | Lys | Leu | Gln | Glu | Tyr | Gln | Ser | Ala | Ile | Lys | Val | Glu | Pro |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Ala | Ser | Pro | Pro | Tyr | Ser | Glu | Lys | Thr | Gln | Leu | Tyr | Asn | Arg | Pro | |
| | | | | 85 | | | | 90 | | | | | 95 | | |
| His | Glu | Glu | Pro | Ser | Asn | Ser | Leu | Met | Ala | Ile | Glu | Cys | Arg | Val | Cys |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Gly | Asp | Lys | Ala | Ser | Gly | Phe | His | Tyr | Gly | Val | His | Ala | Cys | Glu | Gly |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Cys | Lys | Gly | Phe | Phe | Arg | Arg | Thr | Ile | Arg | Leu | Lys | Leu | Ile | Tyr | Asp |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Arg | Cys | Asp | Leu | Asn | Cys | Arg | Ile | His | Lys | Lys | Ser | Arg | Asn | Lys | Cys |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Gln | Tyr | Cys | Arg | Phe | Gln | Lys | Cys | Leu | Ala | Val | Gly | Met | Ser | His | Asn |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Ala | Ile | Arg | Phe | Gly | Arg | Met | Pro | Gln | Ala | Glu | Lys | Glu | Lys | Leu | Leu |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Ala | Glu | Ile | Ser | Ser | Asp | Ile | Asp | Gln | Leu | Asn | Pro | Glu | Ser | Ala | Asp |
| | 195 | | | | | | 200 | | | | | 205 | | | |
| Leu | Arg | Ala | Leu | Ala | Lys | His | Leu | Tyr | Asp | Ser | Tyr | Ile | Lys | Ser | Phe |
| 210 | | | | | 215 | | | | | | 220 | | | | |
| Pro | Leu | Thr | Lys | Ala | Lys | Ala | Arg | Ala | Ile | Leu | Thr | Gly | Lys | Thr | Thr |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Asp | Lys | Ser | Pro | Phe | Val | Ile | Tyr | Asp | Met | Asn | Ser | Leu | Met | Met | Gly |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Glu | Asp | Lys | Ile | Lys | Phe | Lys | His | Ile | Thr | Pro | Leu | Gln | Glu | Gln | Ser |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Lys | Glu | Val | Ala | Ile | Arg | Ile | Phe | Gln | Gly | Cys | Gln | Phe | Arg | Ser | Val |
| | 275 | | | | | | 280 | | | | | 285 | | | |
| Glu | Ala | Val | Gln | Glu | Ile | Thr | Glu | Tyr | Ala | Lys | Asn | Ile | Pro | Gly | Phe |
| 290 | | | | | 295 | | | | | | 300 | | | | |
| Ile | Asn | Leu | Asp | Leu | Asn | Asp | Gln | Val | Thr | Leu | Leu | Lys | Tyr | Gly | Val |
| 305 | | | | 310 | | | | | | 315 | | | | | 320 |
| His | Glu | Ile | Ile | Tyr | Thr | Met | Leu | Ala | Ser | Leu | Met | Asn | Lys | Asp | Gly |
| | | | 325 | | | | | 330 | | | | | 335 | | |
| Val | Leu | Ile | Ser | Glu | Gly | Gln | Gly | Phe | Met | Thr | Arg | Glu | Phe | Leu | Lys |
| | | 340 | | | | | 345 | | | | | 350 | | | |
| Ser | Leu | Arg | Lys | Pro | Phe | Gly | Asp | Phe | Met | Glu | Pro | Lys | Phe | Glu | Phe |
| | 355 | | | | | 360 | | | | | | 365 | | | |
| Ala | Val | Lys | Phe | Asn | Ala | Leu | Glu | Leu | Asp | Asp | Ser | Asp | Leu | Ala | Ile |
| | 370 | | | | 375 | | | | | | 380 | | | | |
| Phe | Ile | Ala | Val | Ile | Ile | Leu | Ser | Gly | Asp | Arg | Pro | Gly | Leu | Leu | Asn |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 |
| Val | Lys | Pro | Ile | Glu | Asp | Ile | Gln | Asp | Asn | Leu | Leu | Gln | Ala | Leu | Glu |
| | | | 405 | | | | | 410 | | | | | 415 | | |
| Leu | Gln | Leu | Lys | Leu | Asn | His | Pro | Glu | Ser | Ser | Gln | Leu | Phe | Ala | Lys |
| | | 420 | | | | | | 425 | | | | 430 | | | |
| Val | Leu | Gln | Lys | Met | Thr | Asp | Leu | Arg | Gln | Ile | Val | Thr | Glu | His | Val |
| | 435 | | | | | | 440 | | | | | 445 | | | |
| Gln | Leu | Leu | His | Val | Ile | Lys | Lys | Thr | Glu | Thr | Asp | Met | Ser | Leu | His |
| | 450 | | | | 455 | | | | | | 460 | | | | |
| Pro | Leu | Leu | Gln | Glu | Ile | Tyr | Lys | Asp | Leu | Tyr | | | | | |
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<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

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Glu Lys Pro Lys Cys Ala Lys Cys Leu Lys Asn Asn Trp Glu Cys Arg
25 30 35

tac tct ccc aaa acc aaa agg tct ccg ctg act agg gca cat ctg aca 199
 Tyr Ser Pro Lys Thr Lys Arg Ser Pro Leu Thr Arg Ala His Leu Thr
 40 45 50 55

gaa gtg gaa tca agg cta gaa aga ctg gaa cag cta ttt cta ctg att 247
Glu Val Glu Ser Arg Leu Glu Arg Leu Glu Gln Leu Phe Leu Leu Ile
60 65 70

ttt cct cga gaa gac ctt gac atg att ttg aaa atg gat tct tta cag 295
Phe Pro Arg Glu Asp Leu Asp Met Ile Leu Lys Met Asp Ser Leu Gln
75 80 85

gat ata aaa gca ttg tta aca gga tta ttt gta caa gat aat gtg aat 343
Asp Ile Lys Ala Leu Leu Thr Gly Leu Phe Val Gln Asp Asn Val Asn
90 95 100

aaa gat gcc gtc aca gat aga ttg gct tca gtg gag act gat atg cct 391
Lys Asp Ala Val Thr Asp Arg Leu Ala Ser Val Glu Thr Asp Met Pro
105 110 115

cta aca ttg aga cag cat aga ata agt gcg aca tca tca tcg gaa gag 439
Leu Thr Leu Arg Gln His Arg Ile Ser Ala Thr Ser Ser Ser Glu Glu
120 125 130 135

agt agt aac aaa ggt caa aga cag ttg act gta tcg ccg gaa ttc ccg 487
 Ser Ser Asn Lys Gly Gln Arg Gln Leu Thr Val Ser Pro Glu Phe Pro
 140 145 150

ggg atc cgt cga cgg tac cag ata tca gga tcc tgg cca gct agc tag 535
Gly Ile Arg Arg Arg Tyr Gln Ile Ser Gly Ser Trp Pro Ala Ser *
155 160 165

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<212> PRT

<213> Saccharomyces cerevisiae

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 Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro
 35 40 45
 Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu
 50 55 60
 Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile
 65 70 75 80
 Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu
 85 90 95
 Phe Val Gln Asp Asn Val Asn Lys Asp Ala Val Thr Asp Arg Leu Ala
 100 105 110
 Ser Val Glu Thr Asp Met Pro Leu Thr Leu Arg Gln His Arg Ile Ser
 115 120 125
 Ala Thr Ser Ser Ser Glu Glu Ser Ser Asn Lys Gly Gln Arg Gln Leu
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 Gly Ser Trp Pro Ala Ser Val Ala Arg
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13

<210> 6
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 <212> DNA
 <213> Mus musculus

<400> 6
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23

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 <212> DNA
 <213> Saccharomyces cerevisiae

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17